Amendments to the Claims:

Listing of Claims:

Claims 1-38 (Canceled)

Claim 39 (Currently amended) A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

reproducibly reducing the complexity of said first nucleic acid sample to produce a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments using a selected fragmentation method, ligating adaptor sequences to said fragments, and amplifying at least some of said fragments ligated with said ~~adapter~~ adaptor sequences using a selected amplification method, ~~wherein a computer is used to predict a plurality of the fragments that will be amplified when the first nucleic acid sample is fragmented by a selected fragmentation method and amplified by a selected amplification method~~;

providing a nucleic acid array, wherein a computer system is used to identify polymorphisms that are predicted to be present on fragments that are amplified when the first nucleic acid sample is fragmented by said selected fragmentation method and amplified by said selected amplification method and wherein said array comprises ~~comprising~~ probes to ~~a~~ interrogate the genotype of a plurality of said polymorphisms ~~present on fragments predicted to be present in the second nucleic acid sample, wherein a computer system is used to predict polymorphisms present on fragments in the second nucleic acid sample~~;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

Claim 40 (Previously presented) The method of claim 39 wherein said second nucleic acid sample comprises at least 0.5 % of the fragments in said first nucleic acid sample.

Claim 41 (Previously presented) The method of claim 39 wherein said second nucleic acid sample comprises at least 3 % of the fragments in said first nucleic acid sample.

Claim 42 (Previously presented) The method of claim 39 wherein said second nucleic acid sample comprises at least 12 % of the fragments in said first nucleic acid sample.

Claim 43 (Previously presented) The method of claim 39 wherein said second nucleic acid sample comprises at least 50 % of the fragments in said first nucleic acid sample.

Claim 44 (Previously presented) The method of claim 39 wherein said first nucleic acid sample is DNA.

Claim 45 (Previously presented) The method of claim 39 wherein said first nucleic acid sample is genomic DNA.

Claim 46 (Previously presented) The method of claim 39 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

Claim 47 (Currently amended) The method of claim 39 wherein the steps of fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, and amplifying at least some of said fragments ligated with said adapter sequences are ~~entire method is~~ performed in a single reaction vessel.

Claim 48 (Currently amended) The method of claim 39 wherein said step of fragmenting ~~the~~ said first nucleic acid sample comprises digestion with at least one restriction enzyme.

Claim 49 (Currently amended) The method of claim 39 wherein said step of fragmenting ~~the~~ said first nucleic acid sample comprises digestion with a type IIs endonuclease.

Claim 50 (Previously presented) The method of claim 39 wherein said adaptor sequences comprise PCR primer template sequences.

Claim 51 (Previously presented) The method of claim 39 wherein said adaptor sequences comprise tag sequences.

Claim 52 (Previously presented) The method of claim 39 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

Claim 53 (Previously presented) The method of claim 52 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

Claim 54-56 (Canceled)

Claim 57 (Currently amended) A method of analyzing a first nucleic acid sample comprising:

providing a first nucleic acid sample;

obtaining a second nucleic acid sample by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

generating said second nucleic acid sample by isolating the DNA duplexes released from the magnetic beads by digestion;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

Claim 57 (Previously presented) The method of claim 57 wherein said restriction enzyme is a Class IIs endonuclease.

Claims 59-173 (Canceled)